

Appl. No. : 09/492,709  
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### AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 19, line 3 and ending at page 19, line 10 with the following rewritten paragraph.

-- BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. ~~Assistance in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov.~~

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Please replace the paragraph beginning at page 19, line 22 and ending at page 19, line 30 with the following rewritten paragraph.

-- In one embodiment of the present invention, an operon is dissected to determine which gene or genes are required for proliferation. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), ~~which may also be found on the website [http://www.cifn.unam.mx/Computational\\_Biology/regulondb/](http://www.cifn.unam.mx/Computational_Biology/regulondb/)~~, may be used. to identify the boundaries of operons encoded within microbial genomes. The Regulon DB database can be accessed on the internet by entering the following quoted text, "www.cifn.unam.", in the address bar of a web browser, such as Internet Explorer or Netscape, followed immediately by "mx/Computational\_Biology/regulondb/". A number of techniques that are well known in the art can be used to dissect the operon. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation. --